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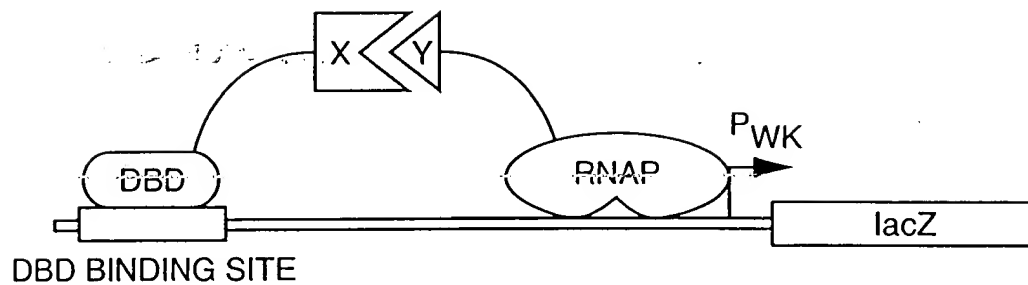


FIG. 1A

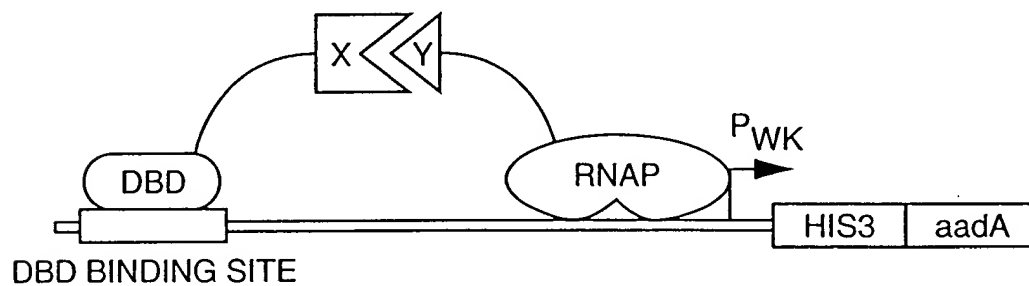


FIG. 1B

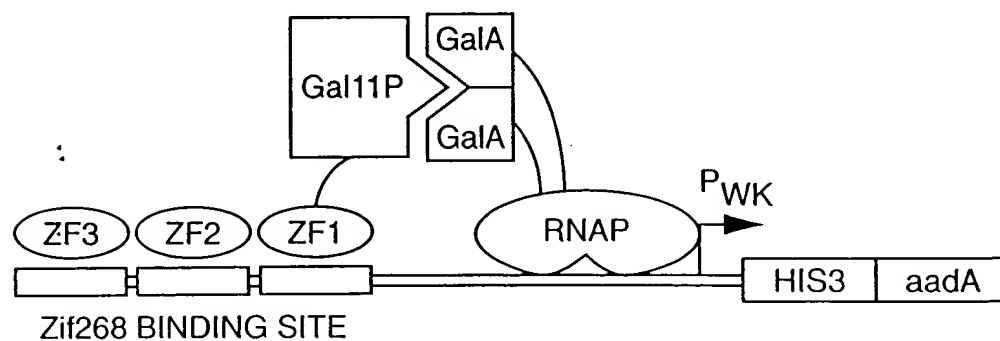


FIG. 1C

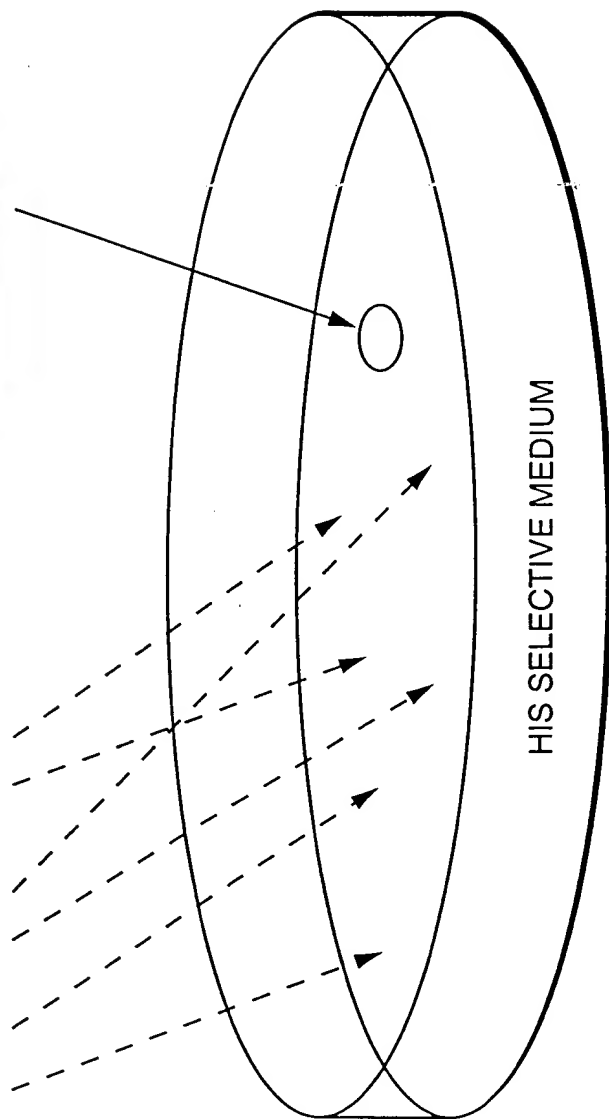
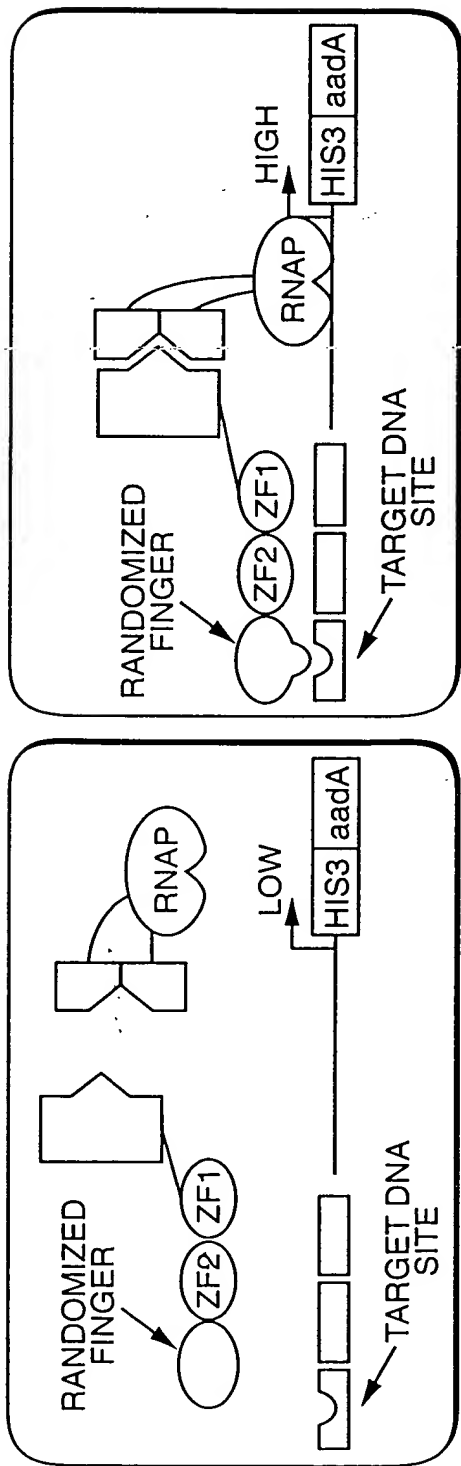
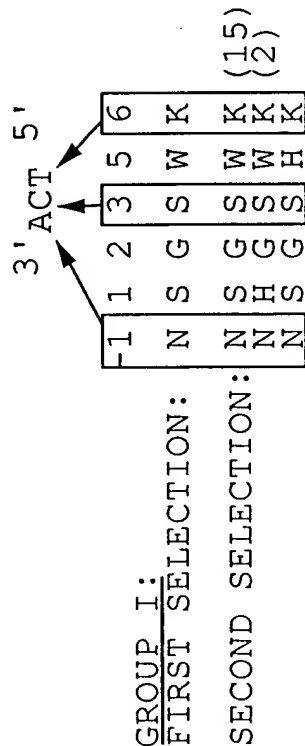


FIG. 2



PHAGE DISPLAY
CONSENSUS:
 T _ T N _ S

FIG. 3C

FROM THE TATA SELECTION:	-1	1	2	3	5	6
	R	R	W	L	K	L
	R	K	W	L	K	L
FROM THE p53 SELECTION:	-1	1	2	3	5	6
	R	K	W	L	K	L
	R	K	W	L	K	L
	R	K	W	L	K	L
FROM THE NRE SELECTION:	-1	1	2	3	5	6
	R	K	W	L	K	L
	R	K	W	L	K	L
	R	K	W	L	K	L

FIG. 3D

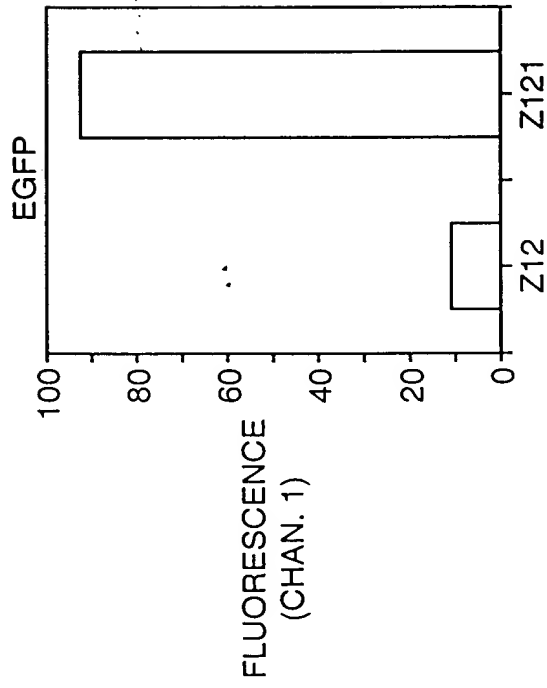


FIG. 4A

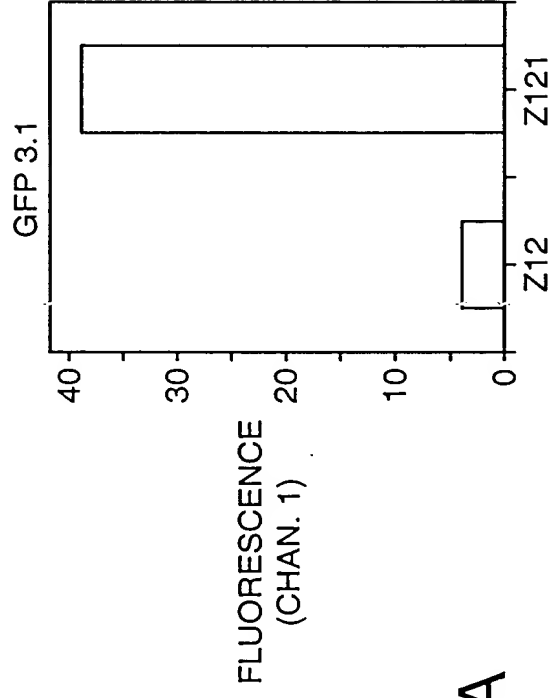


FIG. 4B

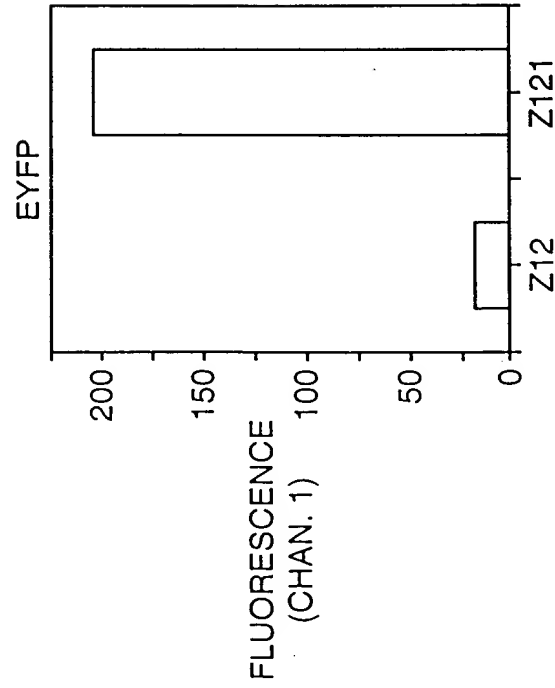


FIG. 4C

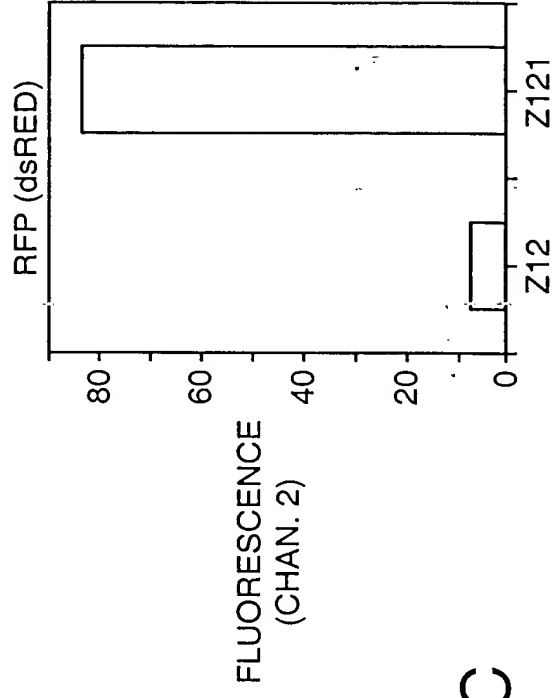


FIG. 4D

09990762.111401

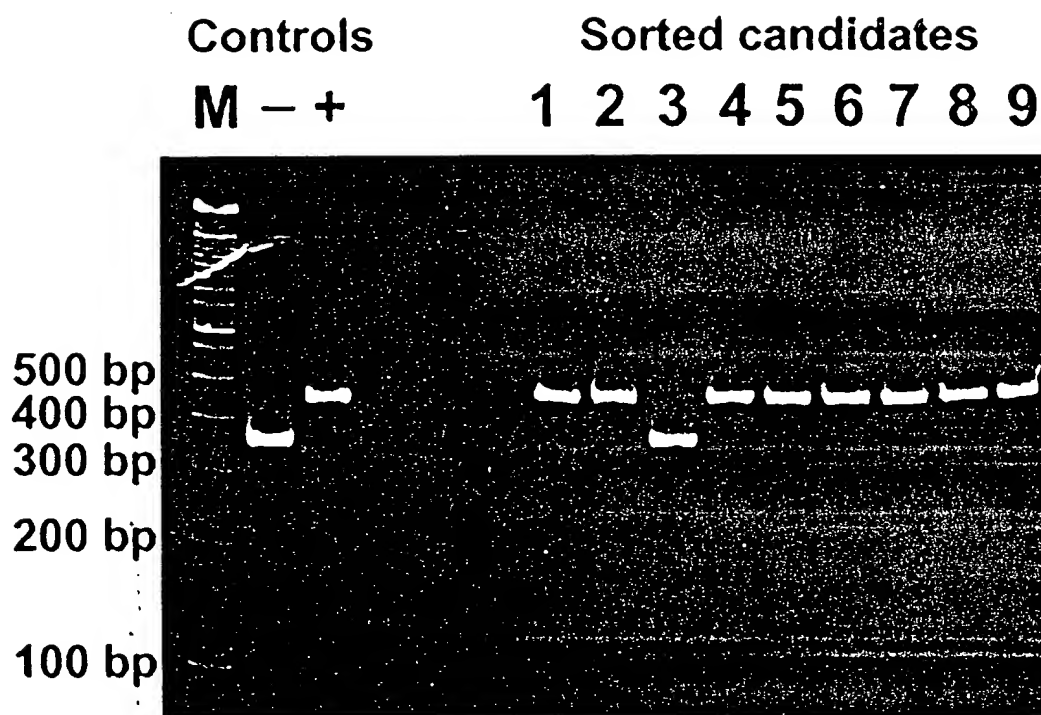


Fig. 5

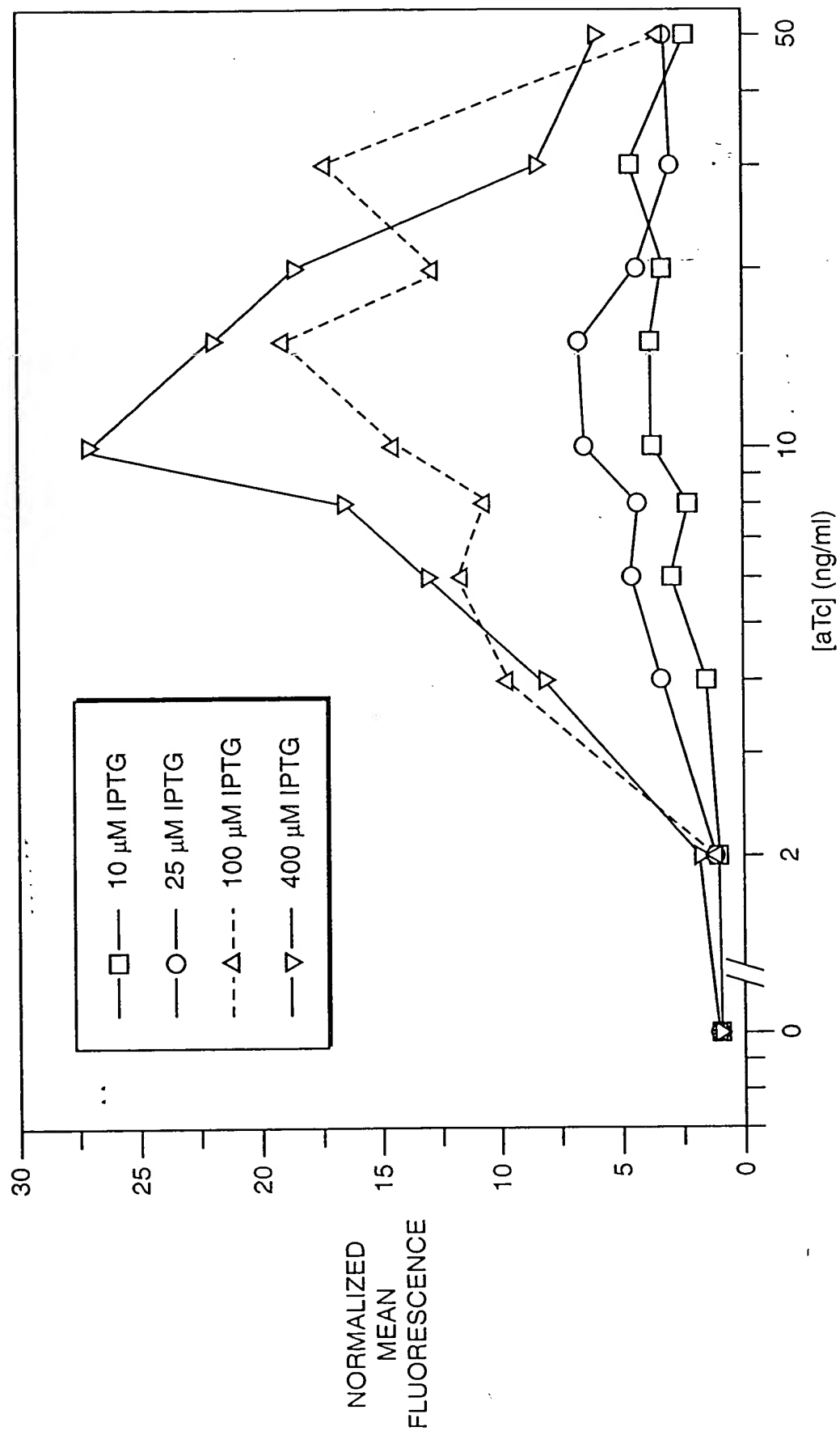


FIG. 6

REPORTER CONSTRUCT #2

REPORTER CONSTRUCT #1

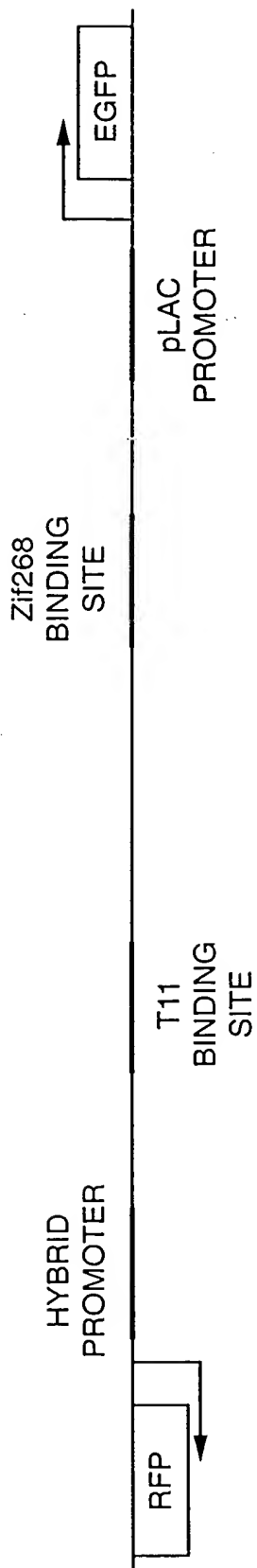


FIG. 7

FIG. 8A

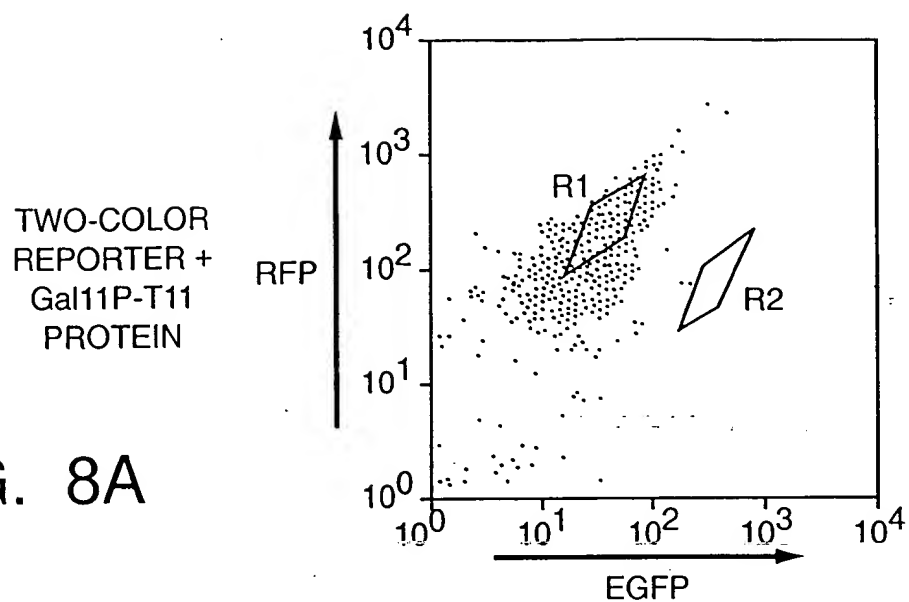


FIG. 8B

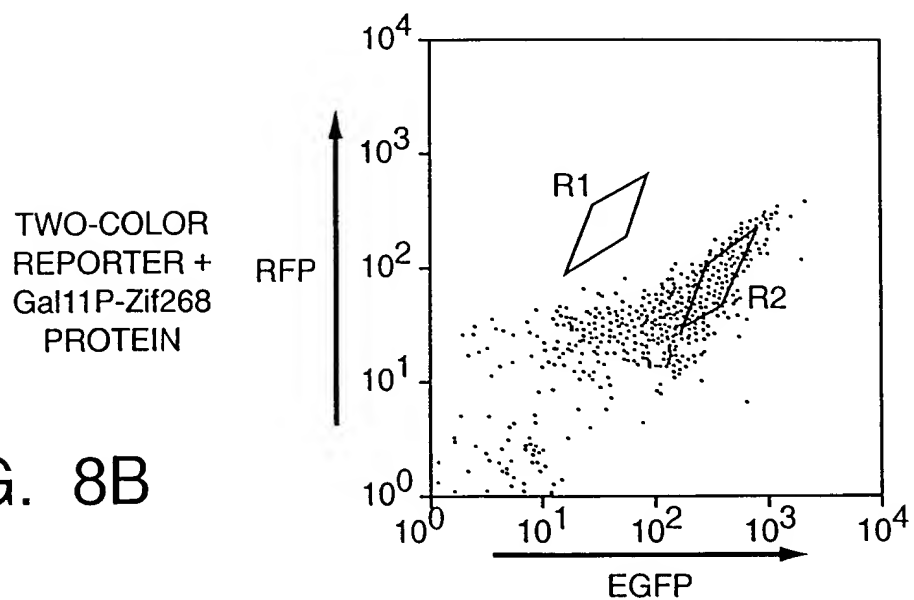
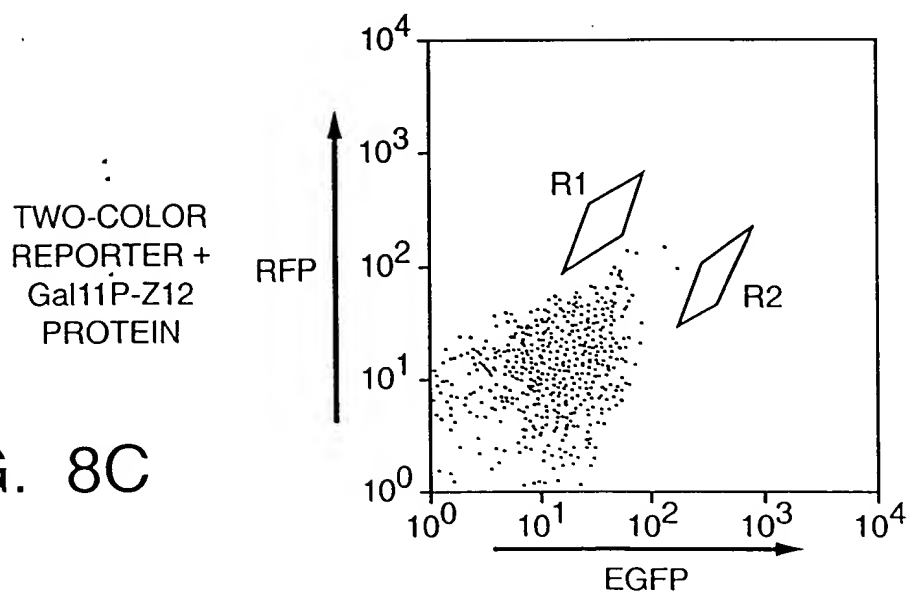


FIG. 8C



0990762-11401

0990762.11401

P53^{ZF} *IN VITRO* SITE SELECTION CONSENSUS SEQUENCE:

CXGGACACGTX

(WHERE X = NO CLEAR PREFERENCE)

IN VIVO SITE SELECTION LIBRARY

CGGGANNNNNNG

(WHERE N = A MIXTURE OF A, G, C, AND T)

SELECTED CLONES:

SEQUENCE	# OF CLONES
CGGGAC <u>AC</u> GTG	9
CGGGAC <u>AT</u> GTG	5
CGGGAC <u>AC</u> G	2

SEQUENCE	FOLD ACTIVATION
CGGGAC <u>AC</u> GTG	18.6 ± 2.7
CGGGAC <u>AT</u> GTG	12.0 ± 0.5
CGGGAC <u>AC</u> G	12.6 ± 1.9

FIG. 9

FIG.10

In vivo site selection

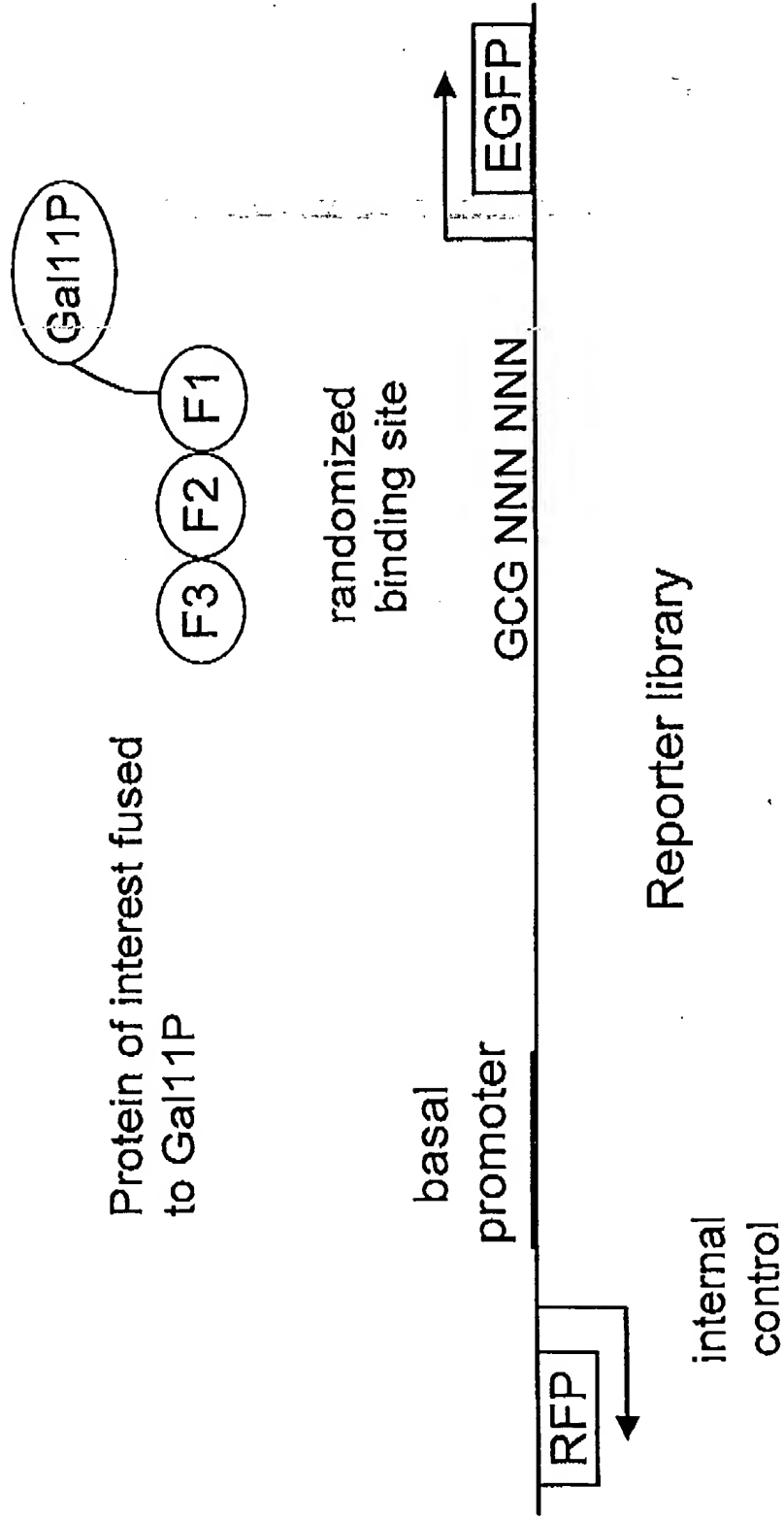


FIG. 11

Selecting Dimerization Domains

Tail to Tail

Variable spacing between sites

Randomized peptides on one monomer can interact with any portion of other monomer, only one possibility is shown

If using FACS version, can use half site driving RFP as counter-selection

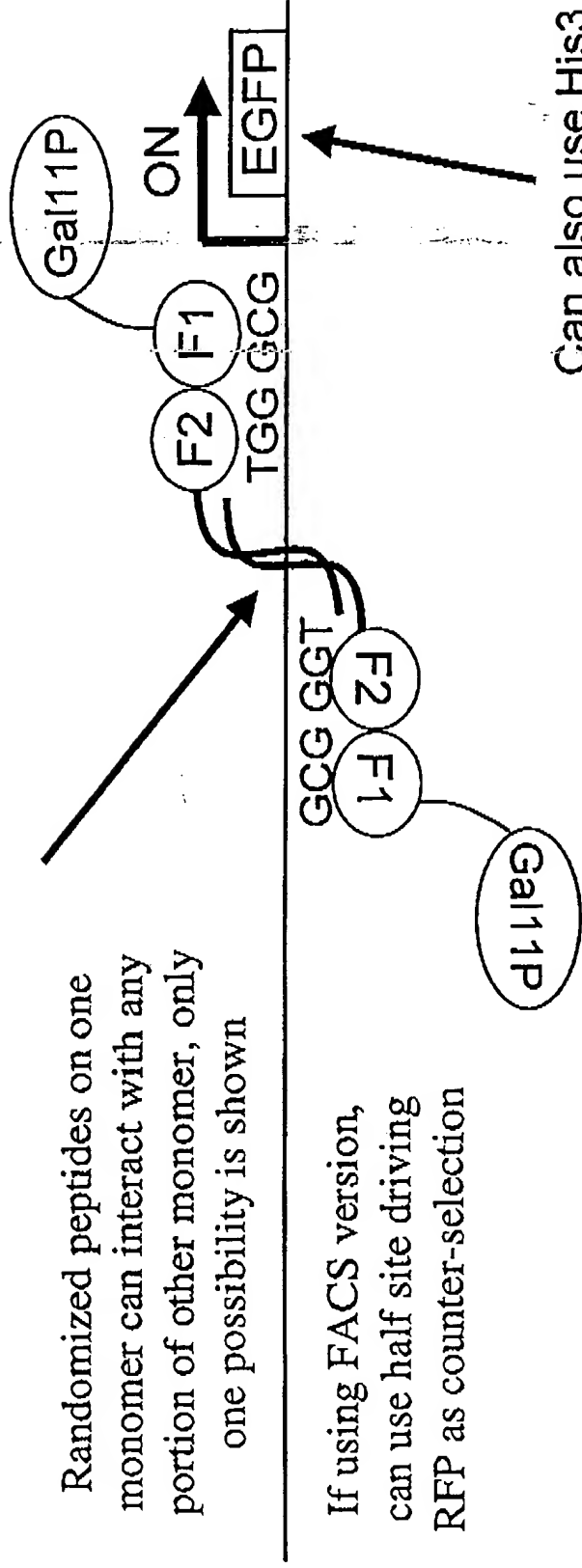
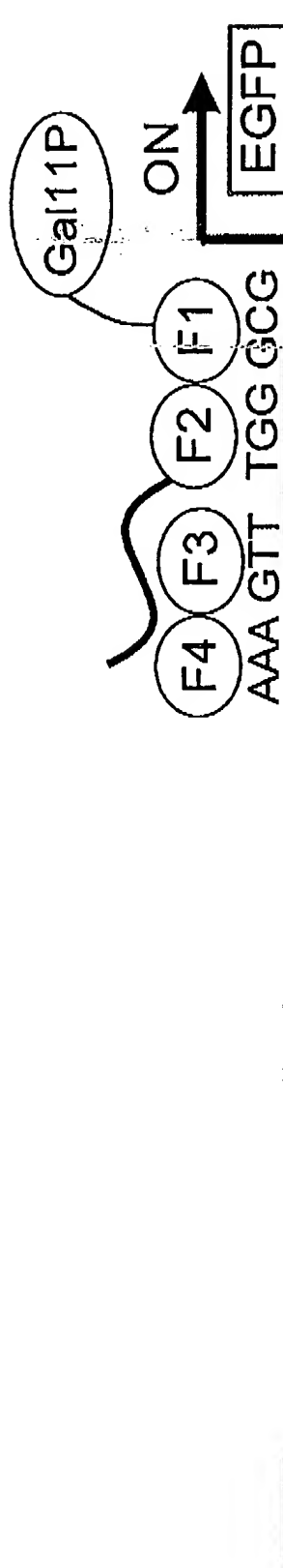


FIG. 12

Selecting Dimerization Domains

Head to Tail



If using FACS version,
can use half site driving
RFP as counter-selection

Can also use His3

Selecting sequence-specific domains from random peptides

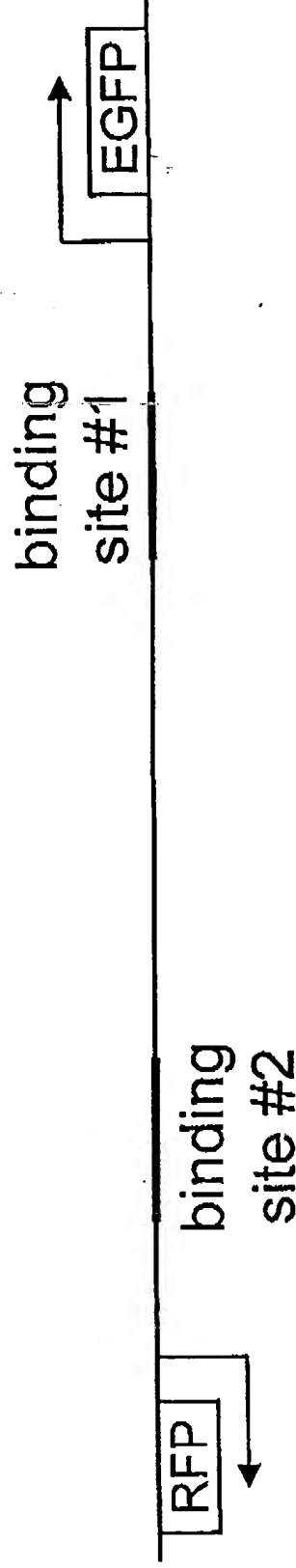
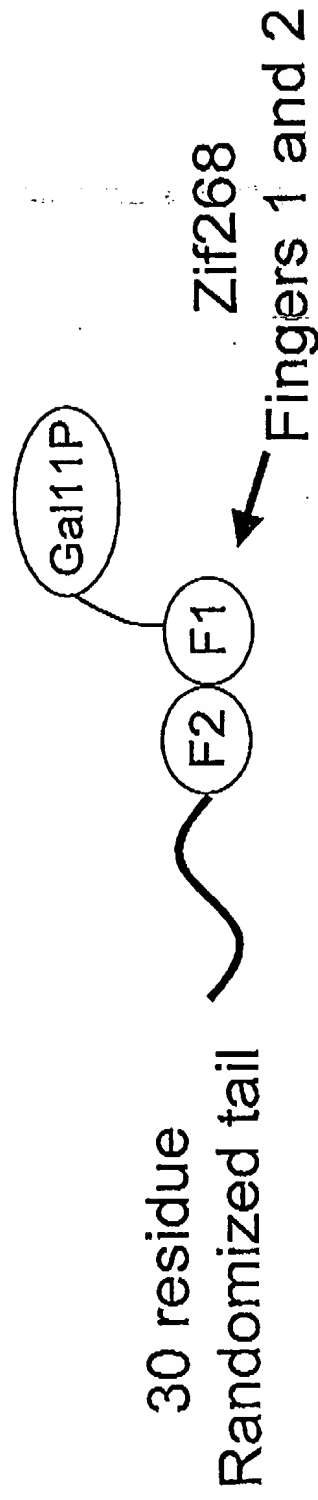


FIG. 14

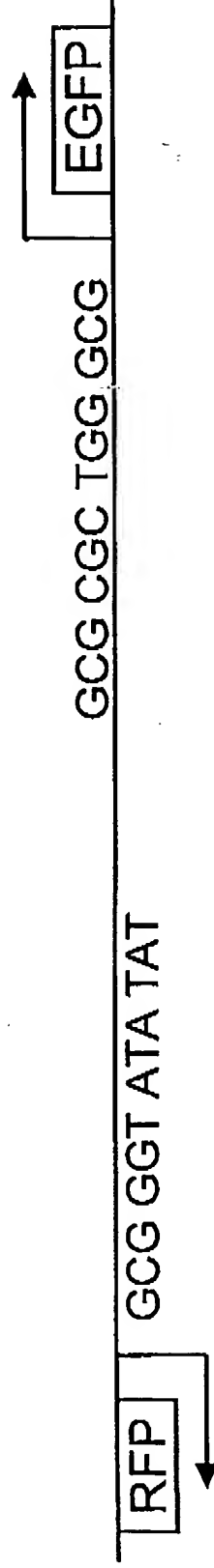
Zif268 finger1

Zif268 finger2

random 30
residue tail

Library size $\sim 2.7 \times 10^8$

Library size $\sim 2.7 \times 10^8$



Sequence of library and reporter

